\_\_\_\_\_\_

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=9; day=4; hr=18; min=4; sec=30; ms=508; ]

\_\_\_\_\_\_

# Validated By CRFValidator v 1.0.3

Application No: 10547206 Version No: 2.0

Input Set:

Output Set:

**Started:** 2008-07-31 16:00:40.207

Finished: 2008-07-31 16:00:42.268

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 61 ms

Total Warnings: 59

Total Errors: 0

No. of SeqIDs Defined: 62

Actual SeqID Count: 62

Error code		Error Description										
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(3)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(4)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(5)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(6)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(7)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(8)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(9)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(10)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(11)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(12)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(13)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(14)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(15)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(16)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(17)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(18)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(19)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(20)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(21)	
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(22)	

### Input Set:

## Output Set:

**Started:** 2008-07-31 16:00:40.207 **Finished:** 2008-07-31 16:00:42.268

**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 61 ms

Total Warnings: 59
Total Errors: 0

No. of SeqIDs Defined: 62

Actual SeqID Count: 62

# Error code Error Description This error has occured more than 20 times, will not be displayed W 402 Undefined organism found in <213> in SEQ ID (59) W 402 Undefined organism found in <213> in SEQ ID (60) W 402 Undefined organism found in <213> in SEQ ID (61)

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<120> Hypoallergenic Der pl and Der p3
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<130> VB60107
<140> 10547206
<141> 2006-05-19
<150> PCT/EP2004/001850
<151> 2004-02-24
<150> 00304424.5
<151> 2003-02-26
<160> 62
<170> FastSEQ for Windows Version 4.0
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<211> 909
<212> DNA
<213> Dermatophagoides pteronyssinus
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accttcgagg acgaggaggc cgcgcgcaag aacttcctgg aaagcgtgaa atacgtgcag 120
agcaacggcg gggctataaa tcacctgtcc gacctgtctt tagacgagtt caagaaccgg 180
ttcctqatqa qcqccqaqqc tttcqaacac cttaaqaccc aqtttqatct caacqcqqaq 240
accaacgect geagtateaa eggeaatgee eeegetgaga ttgatetgeg eeagatgagg 300
accytgactc ccatccycat gcaaggcggc tgcgggtctt gttgggcctt ttcaggcgtg 360
gccgcgacag agtcggcata cctcgcgtat cggaatcaga gcctggacct cgctgagcag 420
gagetegttg aetgegeete eeaacaegga tgteatgggg ataegattee eagaggtate 480
gaatacatcc agcataatgg cgtcgtgcag gaaagctatt accgatacgt agctagggag 540
cagtectgee geogtectaa egeacagege tteggeattt ceaattattg ceagatetae 600
ccccctaatg ccaacaagat cagggaggcc ctggcgcaga cgcacagcgc catcgctgtc 660
atcatcggaa tcaaggatct ggacgcattc cggcactatg acgggcgcac aatcatccag 720
cgcgacaacg gatatcagcc aaactaccac gcggtcaaca tcgtgggtta ctcgaacgcc 780
cagggggtgg actactggat cgtgagaaac agttgggaca ctaactgggg cgacaacggc 840\,
tacggctact tcgccgccaa catcgacctg atgatgatcg aggagtaccc gtacgtggtg 900
atcctgtaa
                                                                   909
<210> 2
<211> 302
<212> PRT
<213> Dermatophagoides pteronyssinus
<400> 2
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1
                 5
                                    10
                                                         15
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Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe

20 25 Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His 40 Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu 70 75 Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu 90 85 Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly 105 100 Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 125 115 120 Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp 135 Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 150 155 Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr 165 170 Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly 180 185 Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg 200 Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 215 220 Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 230 235 Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly 250 245 Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp 265 Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile 280

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu 290 295 300

<210> 3 <211> 302 <212> PRT <213> Artificial Sequence

<220>

<223> Mutant of ProDer P1 C4R (Der P1 numbering)

<400> 3

 Arg
 Pro
 Ser
 Ser
 Ile
 Lys
 Thr
 Phe
 Glu
 Tyr
 Lys
 Lys
 Ala
 Phe
 Ala
 In
 10
 Lys
 Lys
 Lys
 Ala
 Phe
 Ala
 Ala
 Phe
 Ala
 Ala
 Ala
 Phe
 Ala
 Ala
 Ala
 Phe
 Ala
 Ala

Thr Asn Ala Arg Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu

85 90 95

Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
100 105 110

Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu 115 120 125

Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp 130 135 140

Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile 145 150 155 160

Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr 165 170 175

Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
180 185 190

Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg 195 200 205

Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile 210 215 220

Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln 225 230 235 240

Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly 245 250 255

Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp 260 265 270

Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile 275 280 285

Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
290 295 300

<210> 4

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutant of ProDer P1 C4R (Der P1 numbering)

### <400> 4

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```
<220>
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Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
           20
                               25
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
                   7.0
                                       7.5
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
              85
                        90
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Arg Gly
                              105
Ser Cys Trp Ala Phe Ser Gly Val Ala Ala Thr Glu Ser Ala Tyr Leu
       115
                           120
Ala Tyr Arg Asn Gln Ser Leu Asp Leu Ala Glu Gln Glu Leu Val Asp
                       135
                                          140
Cys Ala Ser Gln His Gly Cys His Gly Asp Thr Ile Pro Arg Gly Ile
                   150
                                       155
Glu Tyr Ile Gln His Asn Gly Val Val Gln Glu Ser Tyr Tyr Arg Tyr
              165
                                  170
Val Ala Arg Glu Gln Ser Cys Arg Arg Pro Asn Ala Gln Arg Phe Gly
                              185
Ile Ser Asn Tyr Cys Gln Ile Tyr Pro Pro Asn Val Asn Lys Ile Arg
                           200
Glu Ala Leu Ala Gln Thr His Ser Ala Ile Ala Val Ile Ile Gly Ile
                       215
                                           220
Lys Asp Leu Asp Ala Phe Arg His Tyr Asp Gly Arg Thr Ile Ile Gln
                   230
                                       235
Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly
               245
                                  250
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
                               265
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
                           280
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
                       295
<210> 6
<211> 909
<212> DNA
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<212> PRT

<213> Artificial Sequence

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<213> Artificial Sequence

<223> Mutant of ProDer P1 C31R

<220>

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Arg Asp Asn Gly Tyr Gln Pro Asn Tyr His Ala Val Asn Ile Val Gly

250

255

245

```
Tyr Ser Asn Ala Gln Gly Val Asp Tyr Trp Ile Val Arg Asn Ser Trp
                                2.65
            2.60
Asp Thr Asn Trp Gly Asp Asn Gly Tyr Gly Tyr Phe Ala Ala Asn Ile
                           280
Asp Leu Met Met Ile Glu Glu Tyr Pro Tyr Val Val Ile Leu
    290
                        2.95
                                             300
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<211> 909
<212> DNA
<213> Artificial Sequence
<220>
<223> Mutant of ProDer P1 C65R
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agcaacggcg gggctataaa tcacctgtcc gacctgtctt tagacgagtt caagaaccgg 180
ttcctgatga gcgccgaggc tttcgaacac cttaagaccc agtttgatct caacgcggag 240
accaacqcct qcaqtatcaa cqqcaatqcc cccqctqaqa ttqatctqcq ccaqatqaqq 300
acceptgacte ceateegeat geaaggegge tgegggtett gttgggeett tteaggegtg 360
gccgcgacag agtcggcata cctcgcgtat cggaatcaga gcctggacct cgctgagcag 420
gagetegttg acceptgeete ceaacacgga tgtcatgggg atacgattee cagaggtate 480
gaatacatcc agcataatgg cgtcgtgcag gaaagctatt accgatacgt agctagggag 540
cagtcctgcc gccgtcctaa cgcacagcgc ttcggcattt ccaattattg ccagatctac 600
ccccctaatg ccaacaagat cagggaggcc ctggcgcaga cgcacagcgc catcgctgtc 660
atcatcggaa tcaaggatct ggacgcattc cggcactatg acgggcgcac aatcatccag 720
cgcgacaacg gatatcagcc aaactaccac gcggtcaaca tcgtgggtta ctcgaacgcc 780
cagggggtgg actactggat cgtgagaaac agttgggaca ctaactgggg cgacaacggc 840
tacggctact tcgccgccaa catcgacctg atgatgatcg aggagtaccc gtacgtqqtq 900
                                                                   909
atcctgtaa
<210> 9
<211> 302
<212> PRT
<213> Artificial Sequence
<220>
<223> Mutant of ProDer P1 C71R
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                                    10
Lys Ser Tyr Ala Thr Phe Glu Asp Glu Glu Ala Ala Arg Lys Asn Phe
                                25
Leu Glu Ser Val Lys Tyr Val Gln Ser Asn Gly Gly Ala Ile Asn His
                            4.0
                                                45
Leu Ser Asp Leu Ser Leu Asp Glu Phe Lys Asn Arg Phe Leu Met Ser
Ala Glu Ala Phe Glu His Leu Lys Thr Gln Phe Asp Leu Asn Ala Glu
                    70
                                        75
Thr Asn Ala Cys Ser Ile Asn Gly Asn Ala Pro Ala Glu Ile Asp Leu
                85
                                    90
Arg Gln Met Arg Thr Val Thr Pro Ile Arg Met Gln Gly Gly Cys Gly
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105

110

100

Ser	Суз	Trp	Ala	Phe	Ser	Gly	Val	Ala	Ala	Thr	Glu	Ser	Ala	Tyr	Leu
		115					120					125			
Ala	Tyr	Arg	Asn	Gln	Ser	Leu	Asp	Leu	Ala	Glu	Gln	Glu	Leu	Val	Asp
	130					135					140				
Суз	Ala	Ser	Gln	His	Gly	Arg	His	Gly	Asp	Thr	Ile	Pro	Arg	Gly	Ile
145					150					155					160
Glu	Tyr	Ile	Gln	His	Asn	Gly	Val	Val	Gln	Glu	Ser	Tyr	Tyr	Arg	Tyr
				165					170					175	
Val	Ala	Arg	Glu	Gln	Ser	Cys	Arg	Arg	Pro	Asn	Ala	Gln	Arg	Phe	Gly
			180					185					190		
Ile	Ser	Asn	Tyr	Суз	Gln	Ile	Tyr	Pro	Pro	Asn	Val	Asn	Lys	Ile	Arg
		195					200					205			
Glu	Ala	Leu	Ala	Gln	Thr	His	Ser	Ala	Ile	Ala	Val	Ile	Ile	Gly	Ile
	210					215					220				
Lys	Asp	Leu	Asp	Ala	Phe	Arg	His	Tyr	Asp	Gly	Arg	Thr	Ile	Ile	Gln
225					230					235					240
Arg	Asp	Asn													